

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 12:20:59 : Search time 21 Seconds
(Without alignments) 2512.050 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 549

Sequence: 1 MARRLEPFLCPGGGKAQLS.....EDDLVSHVDSVISRREMYV 549

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : 1
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	322	58.7	407	2	T08732	hypothetical prote
2	100	1.5	106	2	H71133	hypothetical prote
3	106	1.5	106	2	T06479	proline/leucine-tr
4	132	1.5	132	2	A55410	Ig light chain V r
5	266	1.5	266	2	G83178	conserved hypochet
6	293	1.5	293	2	S47094	hypothetical prote
7	341	1.5	341	2	C83578	hypothetical prote
8	342	1.5	342	2	T45456	probable membrane
9	342	1.5	342	2	JC7110	brain-specific mem
10	452	1.5	452	2	T29618	hypothetical prote
11	459	1.5	459	1	KCHUT	interstitial colla
12	470	1.5	470	2	A91804	transmembrane effl
13	503	1.5	503	2	B81690	transmembrane effl
14	503	1.5	503	2	C71535	probable sodium-tr
15	513	1.5	513	2	D88991	probable MADH (ubi
16	594	1.5	594	2	I56248	receptor tyrosine
17	594	1.5	594	2	I58386	receptor tyrosine
18	606	1.5	606	2	T11909	MADH dehydrogenase
19	606	1.5	606	2	T11909	receptor tyrosine
20	607	1.5	607	2	I37560	probable tyrosine k
21	694	1.5	694	2	A95866	probable transketol
22	743	1.5	743	2	E87386	periplasmic beta-g
23	761	1.5	761	2	T03719	probable thyroid r
24	787	1.5	787	2	S68699	potassium channel
25	920	1.5	920	2	T10052	aminopeptidase (EC
26	1309	1.5	1309	1	S35484	peptidyl-dipeptida
27	1622	1.3	1622	2	JE0378	DNA (cytosine-5'-)
28	51	1.3	51	2	S64676	acetylcholinestera
29	87	1.3	87	2	A81232	30S ribosomal prot

30	7	1.3	89	2	A82718	30S ribosomal prot
31	7	1.3	101	2	C95992	hypothetical prote
32	7	1.3	105	1	S15436	ribosomal protein
33	7	1.3	108	2	T26880	hypothetical prote
34	7	1.3	111	1	R85512	ribosomal protein
35	7	1.3	116	2	E72509	probable non speci
36	7	1.3	124	2	D89895	conserved hypotet
37	7	1.3	128	2	AD1509	hypothetical prote
38	7	1.3	134	2	AD0959	secretin precursor
39	7	1.3	135	2	C96844	hypothetical prote
40	7	1.3	135	2	S67324	spore-wall fungal
41	7	1.3	136	2	T15207	hypothetical prote
42	7	1.3	141	2	G83312	probable type II :
43	7	1.3	142	2	A89836	hypothetical prote
44	7	1.3	155	2	D83098	conserved hypotet
45	7	1.3	155	2	C83132	hypothetical prote
46	7	1.3	157	2	D31327	IgE receptor alpha
47	7	1.3	161	2	JC4728	mob protein B - Er
48	7	1.3	166	2	T49489	related to Hr-tran
49	7	1.3	175	2	E72262	conserved hypotet
50	7	1.3	178	2	B71824	hypothetical prote
51	7	1.3	181	2	B84121	hypothetical prote
52	7	1.3	182	2	JC7236	receptor-activity-
53	7	1.3	185	2	S76991	hypothetical prote
54	7	1.3	189	2	JC7262	receptor activity
55	7	1.3	197	2	H81007	phosphohexose iso
56	7	1.3	202	2	A48486	orfX in mob region
57	7	1.3	202	2	C70650	hypothetical prote
58	7	1.3	209	2	H83133	hypothetical prote
59	7	1.3	212	2	A25856	ubiquitin thiolest
60	7	1.3	223	2	JX0222	probable membrane
61	7	1.3	234	2	F95952	fls119and - huma
62	7	1.3	235	2	T38440	insulin-like growt
63	7	1.3	240	2	A39842	hypothetical prote
64	7	1.3	242	2	C95888	hypothetical prote
65	7	1.3	244	2	T04700	IgE receptor alpha
66	7	1.3	245	2	A30154	hypothetical prote
67	7	1.3	245	2	T26868	hypothetical prote
68	7	1.3	247	2	G83705	IgE FC receptor al
69	7	1.3	250	2	A34342	probable COI intro
70	7	1.3	251	2	T07187	conserved hypotet
71	7	1.3	257	2	C69230	hypothetical prote
72	7	1.3	268	2	A13189	cobaltin synthase
73	7	1.3	269	2	W75576	hypothetical prote
74	7	1.3	273	2	T12793	hypothetical prote
75	7	1.3	279	2	T29453	hypothetical prote

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp56B0846.1 - human (fragment)
C:Species: Homo sapiens (homo)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C:Accession: T08732
R:Ottenweider, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OT>
A:Cross-references: EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZp56B0846
C:Genetics:
A:Note: DKFZp56B0846.1

Query Match 58.7%, Score 322, DB 2, Length 407;
Best Local Similarity 100.0%, Pred. No. 1,7e-303;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 143 SGKICAAVFPFGNQSSTVTVLVEPTVSLIKGPDLCIDGNETVAICIAATKAPVA 202

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|||||
Db 1 SGKRYKAVTFPLGNASSITVYLVETPSLTKGPDSSIDGNGNTVAICIMATKPPVA 60
OY 203 HIMEGDLGEMSTTSPFNATIIISQYLFPTFRAGRTTCVYKPALEKDYSFI 262
Db 61 HIMEGDLGEMSTTSPFNATIIISQYLFPTFRAGRTTCVYKPALEKDYSFI 120
OY 263 LDIOYAPREVSVTCGDNFVGRKGVNLCNADANPPFRKSVSRDLGMPDGLASDNTL 322
Db 121 LDIOYAPREVSVTCGDNFVGRKGVNLCNADANPPFRKSVSRDLGMPDGLASDNTL 180
OY 323 HFVHPLTFNVSQYICKVTNSLIGORSODKVIYISDPPTTLTQPTIQWHPSTADIEDLAT 382
Db 181 HFVHPLTFNVSQYICKVTNSLIGORSODKVIYISDPPTTLTQPTIQWHPSTADIEDLAT 240
OY 383 EPKKLPPLSTLATIKDDTITATIASVVGALFIVYVSLAGTCYRRRRFGDYFAAN 442
Db 241 EPKKLPPLSTLATIKDDTITATIASVVGALFIVYVSLAGTCYRRRRFGDYFAAN 300
OY 443 YIPPSDMQKESQIDVLQODELD 464
Db 301 YIPPSDMQKESQIDVLQODELD 322

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RESULT 2

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H71133
hypothetical protein PH0836 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: H71133
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:9834437
A:Accession: H71133
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-100 <KAN>
A:Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29930.1; PID:g3257247
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by Genbank
C:Genetics:
A:Gene: PH0836
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0836

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Query Match

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Best Local Similarity 1.5%; Score 8; DB 2; Length 100;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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41 LLLFPLL 48
|||||
Db 71 LLLFPLL 78

```

RESULT 3

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T06479
proline/leucine-rich protein precursor - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Nov-1999
C:Accession: T06479
R:Rodriguez-Concepcion, M.; Perez-Garcia, A.; Beitran, J.
submitted to the EMBL Data Library, November 1995
A:Description: Isolation of cDNAs which accumulate during pea (Pisum sativum L.) early
A:Reference number: Z15708
A:Accession: T06479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-106 <ROD>
A:Cross-references: EMBL:Z67873; NID:g1213129; PIDN:CAA91780.1; PID:e208966
A:Domain: signal sequence #status predicted <SIG>
A:Product: proline/leucine-rich protein #status predicted <MAT>

```

```

Query Match 1.5%; Score 8; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 36 PPPLLL 43
|||||
Db 79 PPPLLL 86

```

RESULT 4

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A55410
Ig light chain V region (variant CA2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: A55410
R:Tachibana, H.; Kido, I.; Murakami, H.
J. Biol. Chem. 269, 29061-29066, 1994
A:Title: Heterogeneous expression of human antibody lambda chains by concanavalin A
A:Reference number: A55410; MUID:95050725
A:Accession: A55410
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <TAC>
A:Cross-references: GB:S74107
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMH>

```

Query Match

```

Best Local Similarity 1.5%; Score 8; DB 2; Length 132;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 41 LLLFPLL 48
|||||
Db 6 LLLFPLL 13

```

RESULT 5

```

G83178
conserved hypothetical protein PA3747 [imported] - Pseudomonas aeruginosa (strain PA
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83178
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.
adman, S.; Yuan, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.;
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A:Reference number: A82950; MUID:20437337
A:Accession: G83178
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <STO>
A:Cross-references: GB:AE004793; GB:AE004091; NID:g9949904; PIDN:AA607134.1; GSPDB:G
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3747

```

Query Match

```

Best Local Similarity 1.5%; Score 8; DB 2; Length 266;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 39 LLLLFPL 46
|||||
Db 92 LLLLFPL 99

```

RESULT 6

```

S47094
hypothetical protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47094

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OM protein - protein search, using sw model

Run on: November 4, 2002, 12:02:17 ; Search time 6.76126 Seconds
(without alignments)
2021.309 Million cell updates/sec

Title: US-09-972-268-6_COPY_74_152

Perfect score: 416
Sequence: 1 VELKCLIEVNETITQISWEK.....ITLHNIGFSDSKYICAKVT 79

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: SP:archaea:*, 2: SP:bacteria:*, 3: SP:fungi:*, 4: SP:human:*, 5: SP:invertebrate:*, 6: SP:mammal:*, 7: SP:mhc:*, 8: SP:organelle:*, 9: SP:phage:*, 10: SP:plant:*, 11: SP:rodent:*, 12: SP:virus:*, 13: SP:vertebrate:*, 14: SP:unclassified:*, 15: SP:virus:*, 16: SP:bacteriophage:*, 17: SP:archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	416	100.0	549	4 Q9N0S3	Q9N0S3 homo sapien
2	410	98.6	438	11 Q9JLB7	Q9JLB7 mus musculu
3	410	98.6	510	11 Q9JLB8	Q9JLB8 mus musculu
4	410	98.6	549	11 Q9D006	Q9D006 mus musculu
5	410	98.6	549	11 Q9JLB9	Q9JLB9 mus musculu
6	137	32.9	295	6 Q9GJ75	Q9GJ75 bos taurus
7	132	31.7	295	11 Q9GJ75	Q9GJ75 bos taurus
8	131.5	31.6	298	6 Q9GJ74	Q9GJ74 cercoptithec
9	114.5	27.5	261	11 Q9D6A9	Q9D6A9 mus musculu
10	114.5	27.5	408	11 Q9JWP1	Q9JWP1 mus musculu
11	109.5	26.3	336	6 Q15762	Q15762 homo sapien
12	109.5	26.3	336	6 Q46551	Q46551 hylobates s
13	108.5	26.1	336	6 Q18906	Q18906 macaca mula
14	103	24.8	271	12 Q9A3J3	Q9A3J3 homo sapien
15	103	24.8	271	12 Q40948	Q40948 kaposi's sa
16	103	24.8	348	12 P88963	P88963 kaposi's sa

17	101.5	24.4	510	4 Q96N78	Q96N78 homo sapien
18	101.5	24.4	510	4 Q96K15	Q96K15 homo sapien
19	99	23.8	253	12 Q9NRM1	Q9NRM1 macaca mula
20	98.5	23.7	467	21 Q91Y79	Q91Y79 mus musculu
21	94	22.6	278	11 Q8JYD5	Q8JYD5 mus musculu
22	94	22.6	278	11 Q54816	Q54816 mus musculu
23	94	22.6	278	11 Q54901	Q54901 mus musculu
24	92.5	22.2	412	11 Q9JRIE1	Q9JRIE1 rattus norv
25	92.5	22.2	415	11 Q60977	Q60977 mus musculu
26	91.5	22.0	601	11 Q99M67	Q99M67 mus musculu
27	89.5	21.5	355	11 Q921X7	Q921X7 mus musculu
28	89.5	21.5	360	11 Q9D1G9	Q9D1G9 mus musculu
29	87.5	21.0	412	11 Q63611	Q63611 rattus norv
30	87.5	21.0	7962	4 Q10465	Q10465 homo sapien
31	85.5	20.6	449	4 Q9UE26	Q9UE26 homo sapien
32	85.5	20.6	479	4 Q96J79	Q96J79 homo sapien
33	83.5	20.1	259	4 Q85532	Q85532 homo sapien
34	82	19.7	417	4 Q86B31	Q86B31 homo sapien
35	82	19.7	1021	13 P79757	P79757 galus gall
36	80	19.2	1379	13 P79701	P79701 coturnix co
37	78.5	18.9	120	12 Q9DHH2	Q9DHH2 yaba-like d
38	78.5	18.9	186	12 Q91MM6	Q91MM6 lumpy skin
39	78.5	18.9	483	11 Q9DBP8	Q9DBP8 mus musculu
40	77.5	18.6	138	13 Q9YHF7	Q9YHF7 ginglymosto
41	77	18.5	310	11 Q9EPK4	Q9EPK4 mus musculu
42	77	18.5	310	11 Q9DBR7	Q9DBR7 mus musculu
43	77	18.5	310	11 Q9D1M9	Q9D1M9 mus musculu
44	77	18.5	318	13 Q91664	Q91664 xenopus lae
45	77	18.5	407	11 Q9D2J4	Q9D2J4 mus musculu

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	549 AA.
Q9N0S3			
ID Q9N0S3			
AC Q9N0S3			
DT 01-OCT-2000 (TEMBREL, 15, Created)			
DT 01-OCT-2000 (TEMBREL, 15, Last sequence update)			
DT 01-DEC-2001 (TEMBREL, 19, Last annotation update)			
DE NECTIN 3.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX NCBI_Taxid:9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Raymond M., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,			
RA Dubreuil P., Lopez M.,			
RT "Human nectin 3/PRN3: A novel member of the PVR/PRR/nectin family that			
RT interacts with afadin."			
RL Gene 0:0-0(2000).			
DR EMBL: AF282874; AAF97597.1; -			
DR InterPro: IPR003599; Ig_			
DR InterPro: IPR003600; Ig_1ike.			
DR InterPro: IPR003006; Ig_MHC.			
DR Pfam: PF00047; Ig_2.			
DR SMART: SMO0409; Ig_1.			
DR SMART: SMO0410; Ig_1ike; 1.			
SO SEQUENCE 549 AA; 61002 MW; 6D1104CCBA49D731 CRC64;			
Query Match	100.0%	Score 416;	DB 4; Length 549;
Best Local Similarity	100.0%	Pred. No. 1e-39;	
Matches 79; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1 VELKCLIEVNETITQISWEKSSQTVAVHHPQYGVSGEYQGRVLFNNYSNDATI 60			
Db 74 VELKCLIEVNETITQISWEKSSQTVAVHHPQYGVSGEYQGRVLFNNYSNDATI 133			
Qy 61 ITLHNIGFSDSKYICAKVT 79			
Db 134 ITLHNIGFSDSKYICAKVT 152			

```
RESULT 2
09JLB7 PRELIMINARY; PRT: 438 AA.
AC 09JLB7;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE CELL ADHESION MOLECULE NECTIN-3 CANMA.
GN PYRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209403; Pubmed-10744716;
RA Satoh-Horikawa K., Nakanoishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RA "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
that shows homophilic and heterophilic cell-cell adhesion
activities."
RT J. Biol. Chem. 275:10291-10299(2000).
RL
DR EMBL: AF195835; AAF63687.1; -.
DR MGD: MGI:1930171; Pvr13.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00409; IG_1.
DR SMART: SM00410; IG_Like; 1.
SO SEQUENCE 438 AA; 47261 MW; 2A0A441E5802FEF CRC64;

Query Match 98.6%; Score 410; DB 11; Length 438;
Best Local Similarity 97.5%; Pred. No. 3, 8e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 60
DB 74 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 133
OY 61 TLHNIGFSDSGKYICKAVT 79
DB 134 TLHNIGFSDSGKYICKAVT 152

RESULT 3
09JLB8 PRELIMINARY; PRT: 510 AA.
AC 09JLB8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE CELL ADHESION MOLECULE NECTIN-3 BETA.
GN PYRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209403; Pubmed-10744716;
RA Satoh-Horikawa K., Nakanoishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RA "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
that shows homophilic and heterophilic cell-cell adhesion
activities."
RT J. Biol. Chem. 275:10291-10299(2000).
RL
DR EMBL: AF195834; AAF63686.1; -.
DR MGD: MGI:1930171; Pvr13.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00409; IG_1.
DR SMART: SM00410; IG_Like; 1.
SO SEQUENCE 349 AA; 60703 MW; 32775CBE7319B32 CRC64;

Query Match 98.6%; Score 410; DB 11; Length 549;
Best Local Similarity 97.5%; Pred. No. 5e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 60
DB 74 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 133
```

```
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00409; IG_1.
DR SMART: SM00410; IG_Like; 1.
SO SEQUENCE 510 AA; 55811 MW; 45CFE6E7B454864 CRC64;

Query Match 98.6%; Score 410; DB 11; Length 510;
Best Local Similarity 97.5%; Pred. No. 4, 6e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 60
DB 74 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 133
OY 61 TLHNIGFSDSGKYICKAVT 79
DB 134 TLHNIGFSDSGKYICKAVT 152

RESULT 4
Q9D006 PRELIMINARY; PRT: 549 AA.
AC Q9D006;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE 2610301B19RIK PROTEIN.
GN 2610301B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE-21085660; Pubmed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kodora K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehne H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pezole G., Quackenbush J.,
RA Schirni L.M., Steadil P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Oxido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Botfeill D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakemoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection."
RT Nature 409:685-690(2001).
RL
RX EMBL: AK011949; BAB27933.1; -.
RX MGD: MGI:1914402; 2610301B19RIK.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00409; IG_1.
DR SMART: SM00410; IG_Like; 1.
SO SEQUENCE 349 AA; 60703 MW; 32775CBE7319B32 CRC64;

Query Match 98.6%; Score 410; DB 11; Length 549;
Best Local Similarity 97.5%; Pred. No. 5e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 60
DB 74 VSUKCLIEVNETIIOISMEKHKSQTVAVHHPOYGFSGVQGEORVLFKNSLNDATI 133
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 13:13:17 ; Search time 21 seconds

(without alignments)
2512.050 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 2901 1 MARLRPSPLCRGGKAKLS.....EDDLVSHVDGYSIRREMY 549

Sequence: 1 MARLRPSPLCRGGKAKLS.....EDDLVSHVDGYSIRREMY 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2141	73.8	407	2 T08732	hypothetical prote
2	627	21.6	518	2 UC4024	poliovirus recepto
3	494	17.0	467	1 HLMSP3	poliovirus recepto
4	470	16.2	530	2 A53437	poliovirus recepto
5	463.5	16.0	478	2 I53460	PRR2 alpha - human
6	449.5	15.5	538	2 I68093	PRR2 delta - human
7	422.5	14.6	417	2 A44194	poliovirus recepto
8	415.5	14.3	392	2 B44194	poliovirus recepto
9	390.5	13.5	392	1 RMRUPD	poliovirus recepto
10	390.5	13.5	417	1 RMRUPD	poliovirus recepto
11	331.5	11.4	416	2 A54017	colon carcinoma as
12	230.5	7.9	764	2 A49448	irregular chlam C
13	216.5	7.3	4391	2 A38096	perlecan precursor
14	201	6.9	5179	2 T20992	hypothetical prote
15	201	6.9	5198	2 T43290	hemocentin precurs
16	198	6.8	588	2 JH0506	adhesion molecule
17	194	6.7	588	2 A45254	surface glycoprote
18	189	6.5	853	1 IJUBNC	neural cell adhesi
19	187.5	6.5	274	2 A47639	OX-2 membrane glyc
20	187.5	6.5	7962	2 I38346	elastic titin - hu
21	185	6.4	3707	2 S18552	heparan sulfate pr
22	182	6.3	587	2 JH0464	DM-GRASP precursor
23	181.5	6.3	1896	2 T08851	Down syndrome cell
24	178.5	6.2	847	2 JH0371	B-cell adhesion pr
25	174	6.0	858	1 IJRTNC	neural cell adhesi
26	173.5	6.0	761	1 IJHUNG	neural cell adhesi
27	173	6.0	637	2 B33785	myelin-associated
28	172	5.9	513	2 JCS289	SHP substrate-1 pr
29	171.5	5.9	822	2 B49151	fibroblast growth

30	171	5.9	458	2 S23969	cell-adhesion mole
31	171	5.9	582	1 BNR73S	myelin-associated
32	171	5.9	626	1 BNR73	myelin-associated
33	171	5.9	1259	2 A43425	Bravo/Nr-CAM cell
34	169.5	5.8	1091	1 IJCHNL	neural cell adhesi
35	169	5.8	626	1 A61084	myelin-associated
36	168	5.8	765	2 C42632	cell adhesion mole
37	168	5.8	812	2 B42632	cell adhesion mole
38	168	5.8	932	2 A42632	cell adhesion mole
39	166.5	5.7	822	2 S19947	fibroblast growth
40	166	5.7	739	2 JN0581	vascular cell adhe
41	165	5.7	725	1 IJUSNC	neural cell adhesi
42	165	5.7	1115	1 IJUSNC	neural cell adhesi
43	164.5	5.7	569	2 A46462	T cell activation
44	164	5.7	521	2 JC1508	biliary glycoprote
45	163	5.6	458	1 WMSR1	biliary glycoprote

ALIGNMENTS

RESULT 1

T08732
Hypothetical protein DKFZP566B0846.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 13-Aug-1999

C:Accession: T08732

R:Ottenwälder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: 216474

A:Accession: T08732

A:Molecule type: mRNA

A:Residues: 1-407 <COT>

A:Cross-references: EMBL:AL050071

A:Experimental source: Fetal kidney; clone DKFZP566B0846

C:Genetics:

A:Note: DKFZP566B0846.1

Query Match 73.8%; Score 2141; DB 2; Length 407;
Best Local Similarity 99.3%; Pred. No. 7e-147;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	143	SGKTCATVFPPLGNOSSTVTLVLEPTYSILKGPDSLIDGNETVAALCIANGKPYA	202
DB	1	SGKTCATVFPPLGNOSSTVTLVLEPTYSILKGPDSLIDGNETVAALCIANGKPYA	60
QY	203	HIWEGDLGEMESTTSPNETATIIISQVLEPTAPARGRITCVKHPALEKDIRSFI	262
DB	61	HIWEGDLGEMESTTSPNETATIIISQVLEPTAPARGRITCVKHPALEKDIRSFI	120
QY	263	LDIOAPEVSVTGDNMFVGRKGVNLCNADANPPFKSVWSRLDCOMPGLIASDNTL	322
DB	121	LDIOAPEVSVTGDNMFVGRKGVNLCNADANPPFKSVWSRLDCOMPGLIASDNTL	180
QY	323	HEVPLTFNFSYVTKYKNSLGRSDQKVIYISDPPTTLLOPIMHSTADIDLAT	382
DB	181	HEVPLTFNFSYVTKYKNSLGRSDQKVIYISDPPTTLLOPIMHSTADIDLAT	240
QY	383	EPKLPPLSTLTIKDTIATIIASVSGALFIVLVSLAGIFCYRRRTFGDYFANX	442
DB	241	EPKLPPLSTLTIKDTIATIIASVSGALFIVLVSLAGIFCYRRRTFGDYFANX	300
QY	443	YLPSPQKQKSDIVLOQDELSYFDSVKKNKPNVNLIRKDYLEPEKTONNENLN	502
DB	301	YLPSPQKQKSDIVLOQDELSYFDSVKKNKPNVNLIRKDYLEPEKTONNENLN	360
QY	503	REPRNDIYEDLMKMKYSDSHDENEDDLVSHVUGSVISREMY 549	
DB	361	REPRNDIYEDLMKMKYSDSHDENEDDLVSHVUGSVISREMY 407	
RESULT 2	JC4024		

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OM protein - protein search, using sw model

Run on: November 4, 2002, 13:13:37 : Search time 32 Seconds
(without alignments)

2967.944 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 2901
Sequence: 1 MARIKPSPLCPGGSKAQLS.....EDLVSHVDSVISREMYV 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

1 number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1
1: SP_Archaea:.*
2: SP_Bacteria:.*
3: SP_Fungi:.*
4: SP_Human:.*
5: SP_Invertebrate:.*
6: SP_Mammal:.*
7: SP_MHC:.*
8: SP_Organella:.*
9: SP_Phage:.*
10: SP_Plant:.*
11: SP_Protist:.*
12: SP_Virus:.*
13: SP_Vertebrate:.*
14: SP_Unclassified:.*
15: SP_Virus:.*
16: SP_Bacteriophage:.*
17: SP_Archaea:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2901	100.0	549	4 Q9NOS3	Q9NOS3 homo sapien
2	2721	93.8	549	1 Q9JLB9	Q9JLB9 mus musculu
3	2677	92.3	549	11 Q9D006	Q9D006 mus musculu
4	2141	73.8	407	4 Q9Y412	Q9Y412 homo sapien
5	1814.5	62.5	510	11 Q9JLB8	Q9JLB8 mus musculu
6	1809.5	62.4	438	11 Q9JLB7	Q9JLB7 mus musculu
7	1639	56.2	304	4 Q9RVA9	Q9RVA9 mus sapien
8	544	18.8	510	4 Q96NY8	Q96NY8 homo sapien
9	534.5	18.7	510	4 Q96K15	Q96K15 homo sapien
10	528	18.2	295	6 Q9ERF5	Q9ERF5 mesocricetu
11	526.5	18.1	295	6 Q9G174	Q9G174 cercopitheci
12	496	17.1	99	11 Q9CTB0	Q9CTB0 mus musculu
13	494	17.0	467	11 Q9JLV9	Q9JLV9 mus musculu
14	493.5	17.0	483	11 Q9DBR8	Q9DBR8 mus musculu
15	463	16.0	479	4 Q96J29	Q96J29 homo sapien

17	432	14.5	449	4 Q9UE16	Q9UE16 homo sapien
18	413.5	14.3	412	11 Q9RIE1	Q9RIE1 rattus norv
19	408.5	14.1	412	11 Q63611	Q63611 rattus norv
20	400.5	13.8	401	6 Q08835	Q08835 cercopitheci
21	393	13.5	408	11 Q91WP1	Q91WP1 mus musculu
22	390.5	13.5	417	4 Q96B11	Q96B11 homo sapien
23	346	11.9	415	11 Q60977	Q60977 mus musculu
24	337	11.6	494	11 Q9CRY3	Q9CRY3 mus musculu
25	334.5	11.5	442	4 Q9B67	Q9B67 homo sapien
26	271.5	9.4	336	11 Q9D6E7	Q9D6E7 mus musculu
27	250	8.6	261	11 Q9D6A9	Q9D6A9 mus musculu
28	247	8.5	396	11 Q93X28	Q93X28 mus musculu
29	234	8.1	959	5 Q9N9Y9	Q9N9Y9 drosophila
30	234	8.1	968	5 Q9W4T9	Q9W4T9 drosophila
31	233	8.0	306	11 Q9QYL4	Q9QYL4 mus musculu
32	233	8.0	432	4 Q9JUP1	Q9JUP1 homo sapien
33	229.5	7.9	975	5 Q97174	Q97174 drosophila
34	226.5	7.8	295	11 Q9QYL6	Q9QYL6 mus musculu
35	226.5	7.8	295	11 Q9Z2H8	Q9Z2H8 mus musculu
36	218	7.5	278	11 Q9QYL3	Q9QYL3 mus musculu
37	216.5	7.5	4370	4 Q9H3V5	Q9H3V5 homo sapien
38	215	7.4	345	5 Q9MAU1	Q9MAU1 drosophila
39	212.5	7.3	289	11 Q9QYL5	Q9QYL5 mus musculu
40	208	7.2	509	11 Q9QRL5	Q9QRL5 rattus norv
41	207	7.1	509	11 P97710	P97710 rattus norv
42	202	7.0	336	6 Q46551	Q46551 hylobates s
43	202	7.0	5636	4 Q96RW7	Q96RW7 homo sapien
44	201	6.9	5198	5 Q76518	Q76518 caenorhabdi
45	200	6.9	336	6 Q18906	Q18906 macaca mula

ALIGNMENTS

RESULT 1
ID Q9NOS3 PRELIMINARY: PRT; 549 AA.
AC Q9NOS3;
DT 01-OCT-2000 (TREMBLrel, 15, Created)
DT 01-OCT-2000 (TREMBLrel, 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)
DE NECTIN 3
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campedel J., Fiume G.,
RA Dubreuil P., Lopez M.;
RT *Human nectin 3/PER3: A novel member of the PVR/PRR/necln family that
RT interacts with afadin."
RL Gene 0.0-0(2000).
DR EMBL; AF282874; AAF97597.1; -
DR InterPro; IPR003599; IG_ -
DR InterPro; IPR003600; IG_1like.
DR InterPro; IPR003606; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_1.
DR SMART; SM00410; IG_1like; 1.
SO SEQUENCE 549 AA; 61002 MW; 6D1104CBA9D731 CRC64;

Query Match 100.0%; Score 2901; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 7,7e-221;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIKPSPLCPGGKAQLSASLLGAGLLQPTPPULLLLFLLLSRLCSALAGPI 60
1 MARIKPSPLCPGGKAQLSASLLGAGLLQPTPPULLLLFLLLSRLCSALAGPI 60
DB 1 MARIKPSPLCPGGKAQLSASLLGAGLLQPTPPULLLLFLLLSRLCSALAGPI 60
QY 61 IYEPHVAWGNKNSVSKLIEVNETITQISWEKTHGSSQYVAHHPPQYGSVGEYGR 120
61 IYEPHVAWGNKNSVSKLIEVNETITQISWEKTHGSSQYVAHHPPQYGSVGEYGR 120
DB 61 IYEPHVAWGNKNSVSKLIEVNETITQISWEKTHGSSQYVAHHPPQYGSVGEYGR 120

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QY 121 VLEFNNSLNDATITLHNIGFSDSGKYICKAVTTPGLNASSSTTVTVLVEPTVSLKIGPDS 180
DB 121 VLEFNNSLNDATITLHNIGFSDSGKYICKAVTTPGLNASSSTTVTVLVEPTVSLKIGPDS 180
QY 181 LIDGNETVAALCIATGCKPAVHIDMEGDLGEMESTTTSFENETATIIISYKLEPTFRAR 240
DB 181 LIDGNETVAALCIATGCKPAVHIDMEGDLGEMESTTTSFENETATIIISYKLEPTFRAR 240
QY 241 GRRTTCVVKHPALEKDIRSFLLDIQYAPEVSVTGDMVFGKRGVNLCKNDANPPPF 300
DB 241 GRRTTCVVKHPALEKDIRSFLLDIQYAPEVSVTGDMVFGKRGVNLCKNDANPPPF 300
QY 301 KSVWSRLDQWMPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDOKVYIISDPPT 360
DB 301 KSVWSRLDQWMPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDOKVYIISDPPT 360
QY 361 TTTLOPTQWHPSTADIEDLATEPKLPPPLSTLATIKDDTNTITIASVVGALFTVLVS 420
DB 361 TTTLOPTQWHPSTADIEDLATEPKLPPPLSTLATIKDDTNTITIASVVGALFTVLVS 420
QY 421 VLAGIFCYRRRTFRGDIYFPAKNYIPSDMOKESQIDVLQODELDSYPSDKKKNPVNN 480
DB 421 VLAGIFCYRRRTFRGDIYFPAKNYIPSDMOKESQIDVLQODELDSYPSDKKKNPVNN 480
QY 481 LIRKDYLEPEKTOVNNVENLNFRERPMDYEDLKMGMKFVSDENHEDDLVSHVDS 540
DB 481 LIRKDYLEPEKTOVNNVENLNFRERPMDYEDLKMGMKFVSDENHEDDLVSHVDS 540
QY 541 VISREMYV 549
DB 541 VISREMYV 549

RESULT 2
ID 09JLB9 PRELIMINARY: PRT: 549 AA.
AC 09JLB9:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CELL ADHESION MOLECULE NECTIN-3 ALPHA.
GN PVR13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=20289403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RA "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities."
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL: AF195813; AAF63685.1; -.
DR MGI: 1910171; Pvr13.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; Ig_1.
DR SMART: SM00410; Ig_Like_1.
SQ SEQUENCE 549 AA: 60583 MW: 54929AB472F185 CRC64:

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Query Match 93.88: Score 2721; DB 11: Length 549;
Best Local Similarity 92.98; Pred. No. 1.3e-266;
Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
MARTINSPUCGCGGAOISSASLLGALLGPPPPPLLLPLLLFSLRCGALAGPI 60
CGAPLCGCGGCAQLSSAPPAAGLLPAPPPPLLLPLLLFSLRCGALAGSI 60

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QY 61 IVEPHVAVGKNSLKLLEVNETTITQISWEKIGKSGJCVAVHHPQVGSYOGYGR 120
DB 61 IVEPHVAVGKNSLKLLEVNETTITQISWEKIGKSGJCVAVHHPQVGSYOGYGR 120
QY 121 VLEFNNSLNDATITLHNIGFSDSGKYICKAVTTPGLNASSSTTVTVLVEPTVSLKIGPDS 180
DB 121 VLEFNNSLNDATITLHNIGFSDSGKYICKAVTTPGLNASSSTTVTVLVEPTVSLKIGPDS 180
QY 181 LIDGNETVAALCIATGCKPAVHIDMEGDLGEMESTTTSFENETATIIISYKLEPTFRAR 240
DB 181 LIDGNETVAALCIATGCKPAVHIDMEGDLGEMESTTTSFENETATIIISYKLEPTFRAR 240
QY 241 GRRTTCVVKHPALEKDIRSFLLDIQYAPEVSVTGDMVFGKRGVNLCKNDANPPPF 300
DB 241 GRRTTCVVKHPALEKDIRSFLLDIQYAPEVSVTGDMVFGKRGVNLCKNDANPPPF 300
QY 301 KSVWSRLDQWMPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDOKVYIISDPPT 360
DB 301 KSVWSRLDQWMPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDOKVYIISDPPT 360
QY 361 TTTLOPTQWHPSTADIEDLATEPKLPPPLSTLATIKDDTNTITIASVVGALFTVLVS 420
DB 361 TTTLOPTQWHPSTADIEDLATEPKLPPPLSTLATIKDDTNTITIASVVGALFTVLVS 420
QY 421 VLAGIFCYRRRTFRGDIYFPAKNYIPSDMOKESQIDVLQODELDSYPSDKKKNPVNN 480
DB 421 VLAGIFCYRRRTFRGDIYFPAKNYIPSDMOKESQIDVLQODELDSYPSDKKKNPVNN 480
QY 481 LIRKDYLEPEKTOVNNVENLNFRERPMDYEDLKMGMKFVSDENHEDDLVSHVDS 540
DB 481 LIRKDYLEPEKTOVNNVENLNFRERPMDYEDLKMGMKFVSDENHEDDLVSHVDS 540
QY 541 VISREMYV 549
DB 541 VISREMYV 549

RESULT 3
ID 09D006 PRELIMINARY: PRT: 549 AA.
AC 09D006:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE 2610301B19RIK PROTEIN.
DE 2610301B19RIK.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=C57BL/6J; TISSUE=EMBRYO;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh J., Ishi Y.,
RA Araiwa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Imanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli V., Mombaerts P.,
RA Nordone P., Ring B., Ringwald K., Rodriguez I., Sakamoto K.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;

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